

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 16:35:11 ; Search time 10 Seconds
(without alignments)
1078.385 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341
Sequence: 1 MELTQPAEDLIQTQTPASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1341	100.0	260	1 RFXK_HUMAN	Q14593 homo sapien
2	1113.5	83.0	269	1 RFXK_MOUSE	Q92205 mus musculu
3	202.5	15.1	3924	1 ANK2_HUMAN	Q01484 homo sapien
4	193	14.4	4377	1 ANK2_HUMAN	Q12955 homo sapien
5	187	13.9	1337	1 TNK1_HUMAN	Q95271 homo sapien
6	184	13.7	1880	1 ANK1_HUMAN	P16157 homo sapien
7	183	13.6	1862	1 ANK1_MOUSE	Q02357 mus musculu
8	182.5	13.6	231	1 PSDA_MOUSE	Q922X2 mus musculu
9	181.5	13.5	768	1 YB33_HUMAN	Q9137 homo sapien
10	176.5	13.2	226	1 PSDA_HUMAN	Q75833 homo sapien
11	176.5	13.2	231	1 PSDA_MOUSE	Q922X3 ratus norv
12	175	13.0	328	1 ANR2_MOUSE	Q9WV06 mus musculu
13	173	12.9	333	1 ANR2_HUMAN	Q9GZV1 homo sapien
14	172.5	12.9	1059	1 Y379_HUMAN	Q15084 homo sapien
15	169.5	12.6	451	1 ILK_CAVPO	P57044 cavia porce
16	169.5	12.6	741	1 RNSA_HUMAN	Q05823 homo sapien
17	168	12.5	776	1 ANR5_HUMAN	Q9WV02 homo sapien
18	165.5	12.3	452	1 ILK1_HUMAN	Q13418 homo sapien
19	165.5	12.3	452	1 ILK2_HUMAN	P57043 homo sapien
20	164	12.2	642	1 YAZ2_SCHPO	Q99701 mus musculu
21	163.5	12.2	518	1 ASB3_HUMAN	Q9Y575 homo sapien
22	163	12.2	117	1 MTPN_MOUSE	P80144 mus musculu
23	163	12.2	118	1 MTPN_CHICK	Q91955 gallus galli
24	163	12.2	439	1 AKR_ARATH	Q05755 arabidopsi
25	163	12.2	1401	1 LAT2_LATMA	P31631 latrodectus
26	162	12.1	656	1 FEM1_CAEEL	P17221 caenorhadi
27	161	12.0	117	1 MTPN_HUMAN	P58546 homo sapien
28	160.5	12.0	452	1 ILK_MOUSE	O55222 mus musculu
29	160.5	12.0	525	1 ASB3_MOUSE	Q9WV72 mus musculu
30	158.5	11.8	347	1 GABG_MOUSE	O00421 mus musculu
31	158.5	11.8	382	1 GABH_MOUSE	O00420 mus musculu
32	157	11.7	1166	1 TNK2_HUMAN	Q9H2K2 homo sapien
33	157	11.7	775	1 ANR5_MOUSE	Q9d237 mus musculu

34	156.5	11.7	347	1 GABG_HUMAN	O06545 homo sapien
35	156.5	11.7	383	1 GABH_HUMAN	Q06547 homo sapien
36	155	11.6	735	1 RNSA_MOUSE	O05921 mus musculu
37	154	11.5	777	1 BARI_HUMAN	O99728 homo sapien
38	153.5	11.4	592	1 V246_FOWPV	O91424 fowlpox vir
39	152	11.3	587	1 ASB2_HUMAN	O96Q27 homo sapien
40	151	11.3	768	1 BARI_RAT	Q9Q2H2 ratus norv
41	150.5	11.2	168	1 CDN6_HUMAN	P42773 homo sapien
42	149.5	11.1	433	1 AS14_MOUSE	O8VH87 mus musculu
43	149	11.1	227	1 PHLB_SERLI	P18954 serratia 11
44	149	11.1	323	1 ANKH_CHRVI	O06527 chromatium
45	148.5	11.1	765	1 BARI_MOUSE	O70445 mus musculu

ALIGNMENTS

RESULT 1
RFXK_HUMAN STANDARD; PRT; 260 AA.
ID AC Q14593; Q95839;
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-binding protein RFXANK (Regulatory factor X subunit B) (RFX-B).
GN RFXANK OR RFXB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MASS SPECTROMETRY.
RC TISSUE=B-cell;
RX MEDLINE=99021383; PubMed=9606546;
RA Maestriak K., Bartra E., Zufferey M., Conrad B., Corthals G.,
RA Aebbersold R., Sanchez J.-C., Hochreiter D.F., Mach B., Reith W.;
RT "A gene encoding a novel RFX-associated transactivator is mutated in
RL the majority of MHC class II deficiency patients.";
RL Nat. Genet. 20:273-277(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 180-198; 100-210 AND
RP 238-248.
RC TISSUE=Lymphoblast;
RX MEDLINE=99170284; PubMed=10072068;
RA Nagarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
RA Boss J.M.;
RT "RFX-B is the gene responsible for the most common cause of the bare
RL lymphocyte syndrome, a MHC class II deficiency.";
RL Immunity 10:153-162(1999).
RN [3]
RP ERRATUM.
RA Nagarajan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
RA Boss J.M.;
RL Immunity 10:399-399(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Zhou J., Guan Z., Gu J., Ye M., Fu G., Zhang Q., Xu S., He K.,
RA Chen S., Mao M., Chen Z.;
RT "Hematopoiesis-derived ankyrin-like gene";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 65-260 FROM N.A.
RA Lamerdin J.E., McGready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Christensen M., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Gaines J., Dargatzian L., Bruce R., Quan G., Montgomery M., Ow D.,
RA Kobayashi A., Olsen A.O., Carraro A.V.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP VARIANT BLS PRO-195.
RX MEDLINE=20192025; PubMed=10725724;
RA Nagarajan U.M., Peijnenburg A., Gobin S.J., Boss J.M.,
RA van den Elsen P.J.;
RT "Novel mutations within the RFX-B gene and partial rescue of MHC and

RT related genes through exogenous class II transactivator in
RT RFX-B-deficient cells."
RL J. Immunol. 164:3666-3674(2000).
CC -1- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.
CC -1- ACTIVATION REQUIRES THE ACTIVITY OF THE MHC CLASS II
CC TRANSACTIVATOR (CIITA). MAY REGULATE OTHER GENES IN THE CELL. RFX
CC BINDS THE X1 BOX OF MHC-II PROMOTERS. ISOFORM RFX-B-DELTA5 IS NOT
CC INVOLVED IN THE POSITIVE REGULATION OF MHC CLASS II GENES.
CC -1- SUBUNIT: RFX CONSISTS OF AT LEAST THREE DIFFERENT SUBUNITS; RFXAP,
CC RFX5 AND RFX-B/REFXANK, WITH EACH SUBUNIT REPRESENTING A SEPARATE
CC COMPLEMENTATION GROUP. RFX FORMS COOPERATIVE DNA BINDING COMPLEXES
CC WITH X2BP AND CBF/NF-Y. RFX ASSOCIATES WITH CIITA TO FORM AN
CC ACTIVE TRANSCRIPTIONAL COMPLEX.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
CC RFX-B-DELTA5. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- DOMAIN: THE THIRD ANKYRIN REPEAT IS REQUIRED FOR ASSOCIATION WITH
CC THE TWO OTHER RFX SUBUNITS; RFX5 AND RFXAP.
CC -1- DISEASE: DEFECTS IN RFXANK ARE A CAUSE OF HEREDITARY MHC CLASS II
CC DEFICIENCY (ALSO KNOWN AS BARE LYMPHOCYTE SYNDROME (BLS) OR HLA
CC CLASS II-DEFICIENT COMBINED IMMUNODEFICIENCY); A FORM OF SEVERE
CC COMBINED IMMUNODEFICIENCY DISEASE (SCID). RFXANK IS LINKED WITH
CC BLS COMPLEMENTATION GROUP B.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.

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DR EMBL; AF094760; AAC69883.1; -
DR EMBL; AF105427; AAD1972.1; -
DR EMBL; AF105428; AAD1973.1; -
DR EMBL; AF077196; AAD26991.1; -
DR EMBL; AF003110; AAB86654.1; -
DR HSSP; P42773; 1BU9.
DR GeneW; HGNC:9987; RFXANK.
DR MIM; 603200; -
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ank; 3.
DR PROSITE; PSS0088; ANK_REPEAT; 3.
KW DNA-binding; Transcription regulation; Activator; Nuclear protein;
KW Repeat; ANK repeat; Alternative splicing; Phosphorylation;
KW Disease mutation; SCID.
FT REPEAT 89 118 ANK 1.
FT REPEAT 123 152 ANK 2.
FT REPEAT 156 185 ANK 3.
FT REPEAT 189 218 ANK 4.
FT REPEAT 222 251 ANK 5.
FT VARSPLIC 63 63 MISSING (IN ISOFORM RFX-B-DELTA5).
FT VARSPLIC 91 113 SLISHOLAAGSELQLEHLEKRG -> C (IN ISOFORM
FT VARSPLIC 195 195 RFX-B-DELTA5).
FT VARIANT 195 195 L->P (IN BLS).
FT FTID=VAR 009941.
FT FTID=VAR 009941.
SQ SEQUENCE 260 AA; 28102 MW; 62808490F54816D2 CRC64;

DB 61 PQAGSSIKHSTTLTNRORGEVSAIPATLDSLSIHQLAAGELDQKEHLRGDNLVNP 120
QY 121 DERGFPLIASAFGEIETRFLEMGADPHILAKERSALSLASTGGYTDIVGLLEED 180
DB 121 DERGFPLIASAFGEIETRFLEMGADPHILAKERSALSLASTGGYTDIVGLLEED 180
QY 181 VDINIDWNGSTPLLYAVRGNHVCVEALLARGADLTTEADSGYTPMDIALVALGTRKVOQ 240
DB 181 VDINIDWNGSTPLLYAVRGNHVCVEALLARGADLTTEADSGYTPMDIALVALGTRKVOQ 240
QY 241 VIENHILKLFOSNLVPPADPE 260
DB 241 VIENHILKLFOSNLVPPADPE 260
RESULT 2
ID RFXK_MOUSE STANDARD; PRT; 269 AA.
AC Q9Z205;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-binding protein RFXANK (Regulatory factor X subunit B) (RFX-B)
DE (Regulatory factor X-associated ankyrin-containing protein) (Ankyrin
DE repeat-containing adaptor protein TV1-1).
GN RFXANK OR RFXB OR TVL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=99021383; PubMed=9806546;
RA Masternak K., Barras E., Zufferey M., Conrad B., Cortals G.,
RA A gene encoding a novel RFX-associated transactivator is mutated in
RT the majority of MHC class II deficiency patients."
RL Nat. Genet. 20:273-277(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=99262619; PubMed=1039666;
RA Lin J.-H., Makris A., McMahon C., Bear S.E., Patriotic C.,
RA Prasad V.R., Brent R., Golemis E.A., Tschlis P.N.;
RT "The ankyrin repeat-containing adaptor protein tvl-1 is a novel
RT substrate and regulator of raf-1."
RL J. Biol. Chem. 274:14706-14715(1999).
CC -1- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.
CC ACTIVATION REQUIRES THE ACTIVITY OF THE MHC CLASS II
CC TRANSACTIVATOR (CIITA). MAY REGULATE OTHER GENES IN THE CELL (BY
CC SIMILARITY). POTENTIATES THE ACTIVATION OF RAF-1. RFX BINDS THE X1
CC BOX OF MHC-II PROMOTERS.
CC -1- SUBUNIT: RFX CONSISTS OF AT LEAST 3 DIFFERENT SUBUNITS; RFXAP,
CC RFX5 AND RFX-B/REFXANK. RFX FORMS COOPERATIVE DNA BINDING
CC COMPLEXES WITH X2BP AND CBF/NF-Y. RFX ASSOCIATES WITH CIITA TO
CC FORM AN ACTIVE TRANSCRIPTIONAL COMPLEX (BY SIMILARITY). FORMS
CC OLIGOMERS. ASSOCIATES WITH RAF-1.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THYMUS, LUNG AND
CC TESTES.
CC -1- DOMAIN: INTERACTS WITH RAF-1 VIA ITS C-TERMINAL ANKYRIN REPEAT
CC DOMAIN. THE SAME DOMAIN ALSO MEDIATES ITS HOMODIMERIZATION.
CC -1- DOMAIN: THE THIRD ANKYRIN REPEAT IS REQUIRED FOR ASSOCIATION WITH
CC THE TWO OTHER RFX SUBUNITS; RFX5 AND RFXAP (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED BY RAF-1.
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.

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DR EMBL; AF094761; AAC69884.1; -
 DR EMBL; AF123704; AAD24798.1; -
 DR HSSP; P80144; 2MCO.
 DR MGD; MG1:1333865; Rfxank.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 4.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PSS0088; ANK_REPEAT; 3.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 DR DNA-binding; Transcription regulation; Activator; Nuclear protein;
 KW Repeat; ANK repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 88 127 ANK 1.
 FT REPEAT 132 161 ANK 2.
 FT REPEAT 165 194 ANK 3.
 FT REPEAT 198 227 ANK 4.
 FT REPEAT 231 260 ANK 5.
 FT VARSPLIC 112 121 MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 269 AA; 29231 MW; 5713F33DC69EB7 CRC64;

Query Match
 Best Local Similarity 83.0%; Score 1113.5; DB 1; Length 269;
 Matches 221; Conservative 15; Mismatches 23; Indels 11; Gaps 2;

QY 1 MELTQAPEDLIQTQTPASELGPDEPGEAADSPTVVLSTPCTPEPVNPEPPASVSS 60
 Db 1 MEPTQAVENLVNPOQPPVPLEDEPDRSDSPENSPTVLSLFTCTDVAPEADASASS 60
 QY 61 PQAGSLKSTITLTNRQGNVEVALPTLDSLTHQLAAGELDQLEHLNK----- 112
 Db 61 LQ-GSEFLKSTITLTNRQGNVEVALPTLDSLTHQLAAGELSLQLDHLKGCAPACTC 119
 QY 113 --GDNVNPDESGFPLTVASAFGEIETVRLLEMGADPHILAKESASLSTSGYT 170
 Db 120 LSGNNLNPDESGFPLTVASAFGEIETVRLLEMGADPHILAKESASLSTSGYT 179
 QY 171 DIVGLLEEDVDINIDVNGGTPLVAVRGNHVCVALLARGADLTTEADSGYTPMDLA 230
 Db 180 DIVRLLEEDVDINIDVNGGTPLVAVRGNHVCVALLARGADLTTEADSGYTPMDLA 239
 QY 231 VALGTRKVOQVIEHLILKLFQSNLVPADPE 260
 Db 240 VALGYRKVOQVIEHLILKLFQSNLVPADPE 269

RESULT 3
 ANK2_HUMAN
 ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
 AC Q01484; Q01485;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain stem;
 RX MEDLINE=91302466; PubMed=1830053;
 RA Otsu E., Kunimoto M., McLaughlin T., Bennett V.;
 RT "Isolation and characterization of cDNAs encoding human brain
 RT ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253 (1991).
 RN [2]
 RP REVISIONS.
 RA Carpenter S.;

RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain stem;
 RX MEDLINE=94075409; PubMed=8253844;
 RA Chan W., Kordeli E., Bennett V.;
 RT "40-kD ankyrinB: structure of the major developmentally regulated
 RT domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473 (1993).
 RN [4]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE=92009921; PubMed=1833308;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 RT ankyrin gene.";
 RL Genomics 10:858-866 (1991).
 CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
 CC elements. Also bind to cytoskeletal proteins.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CC CELLS THROUGHOUT THE BRAIN.
 CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 CC AND FUNCTION (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 CC EMBL; X56957; CAA40278.1; -
 DR EMBL; X56958; CAA40279.2; -
 DR EMBL; Z26634; CAB24644.1; -
 DR EMBL; M37123; AAA62828.1; -
 DR PIR; S14533; S14533.
 DR PIR; A39643; A39643.
 DR PIR; B39643; B39643.
 DR PIR; S14569; S14569.
 DR HSSP; P42771; IDC2.
 DR Genew: HGNC:493; ANK2.
 DR MTM; 106410; -
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.
 DR PROSITE; PSS0088; ANK_REPEAT; 20.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation.
 FT REPEAT 63 92 ANK 1.
 FT REPEAT 96 125 ANK 2.
 FT REPEAT 129 158 ANK 3.
 FT REPEAT 162 191 ANK 4.
 FT REPEAT 193 220 ANK 5.
 FT REPEAT 232 261 ANK 6.
 FT REPEAT 265 294 ANK 7.
 FT REPEAT 298 327 ANK 8.
 FT REPEAT 331 360 ANK 9.
 FT REPEAT 364 393 ANK 10.


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CC FT VARIANT 844 844 D -> E.
CC FT VARIANT 1285 1285 /FtId=VAR_000599.
CC FT VARIANT 1391 1391 /FtId=VAR_000601.
CC FT VARIANT 1591 1591 /FtId=VAR_000600.
CC FT VARIANT 1698 1698 /FtId=VAR_000602.
CC FT VARIANT 1698 1698 /FtId=VAR_000603.
CC FT CONFLICT 229 229 A -> S (IN REF. 2).
CC FT CONFLICT 1545 1545 V -> I (IN REF. 2).
CC SEQUENCE 1880 AA; 206145 MW; 1CSF5E7EPD1CD428 CRC64;

Query Match 13.7%; Score 184; DB 1; Length 1880;
Best Local Similarity 23.1%; Pred. No. 1.1e-06;
Matches 54; Conservative 37; Mismatches 69; Indels 74; Gaps 3;

QY 74 TNRQGNVSLPATLDSIHOALAQGLDQKELRKGDVNVKPPERGFTPLIMASA 133
DB 72 TTTKGN-----TALHIALAQDEVRRLVNYGAN-VNAQSKGFTPLIMAAQ 119
QY 134 FGEIETVFLLEWGAADPHILAKERESALSLASTGTYDIVG----- 174
DB 120 ENHLEVVKFLLENGANQVATEDGFTPLAVLALQGHENVAHLINVTGKAVRLPALHIA 179
QY 175 -----LLERPDVINDIYDMNGA 191
DB 180 ARNDRTAAVLQNDPNPDLVSKTGFTPLHIAHYENLVNQLLNKRASVNFPTQNGI 239
QY 192 TPLLYAVGNHVKCEALLARGADLTTEADSGYTPMDLVALGYRKVOQVIENH 245
DB 240 TPLHIAARGVIVVRLLDGAGQIETKQDELTPHCAARGHVAISILLDH 293

RESULT 7
ANK1_MOUSE STANDARD; PRT; 1862 AA.
ID ANK1_MOUSE
AC 002357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ankyrin 1 (Erythrocyte ankyrin).
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=92345717; PubMed=1386265;
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.,
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
RT regulatory domain."
RL Mamm. Genome 3:281-285 (1992).
CC -|- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -|- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -|- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -|- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M84756; AAA37236.1; -
CC DR HSSP; Q00420; IABC.
CC DR MGI; MGI:88024; Ank1.
CC DR InterPro; IPR002110; ANK.
CC DR InterPro; IPR000488; Death.
CC DR InterPro; IPR000906; ZUS.
CC DR Pfam; PF00023; ank; 24.
CC DR Pfam; PF00531; death; 1.
CC DR Pfam; PF00791; ZUS; 1.
CC DR PRINTS; PRO1415; ANKYRIN.
CC DR SMART; SM00248; ANK; 22.
CC DR SMART; SM00005; DEATH; 1.
CC DR SMART; SM00218; ZUS; 1.
CC DR PROSITE; P55008; ANK_REPEAT; 20.
CC DR PROSITE; P550297; ANK_REPEAT_REGION; 1.
CC DR PROSITE; P550017; DEATH_DOMAIN; 1.
CC KW Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
CC DOMAIN 1 827 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
CC BINDING DOMAIN).
CC DOMAIN 828 1386 62 KDA DOMAIN (SPECTRIN BINDING
CC DOMAIN).
CC DOMAIN 1387 1862 55 KDA REGULATORY DOMAIN (REGULATES
CC THE BINDING OF ANKYRIN TO SPECTRIN
CC AND THE BAND 3 PROTEIN).
CC FT REPEAT 40 69 ANK 1.
CC FT REPEAT 73 102 ANK 2.
CC FT REPEAT 106 135 ANK 3.
CC FT REPEAT 139 168 ANK 4.
CC FT REPEAT 170 197 ANK 5.
CC FT REPEAT 201 230 ANK 6.
CC FT REPEAT 234 263 ANK 7.
CC FT REPEAT 267 296 ANK 8.
CC FT REPEAT 300 329 ANK 9.
CC FT REPEAT 333 362 ANK 10.
CC FT REPEAT 366 395 ANK 11.
CC FT REPEAT 399 428 ANK 12.
CC FT REPEAT 432 461 ANK 13.
CC FT REPEAT 465 494 ANK 14.
CC FT REPEAT 498 527 ANK 15.
CC FT REPEAT 531 560 ANK 16.
CC FT REPEAT 564 593 ANK 17.
CC FT REPEAT 597 626 ANK 18.
CC FT REPEAT 630 659 ANK 19.
CC FT REPEAT 663 692 ANK 20.
CC FT REPEAT 696 725 ANK 21.
CC FT REPEAT 729 758 ANK 22.
CC FT REPEAT 762 791 ANK 23.
CC FT DOMAIN 1399 1483 DEATH.
CC SEQUENCE 1862 AA; 204242 MW; AEB85B5B29001E5 CRC64;

Query Match 13.6%; Score 183; DB 1; Length 1862;
Best Local Similarity 23.1%; Pred. No. 1.3e-06;
Matches 54; Conservative 36; Mismatches 70; Indels 74; Gaps 3;

QY 74 TNRQGNVSLPATLDSIHOALAQGLDQKELRKGDVNVKPPERGFTPLIMASA 133
DB 69 TTTKGN-----TALHIALAQDEVRRLVNYGAN-VNAQSKGFTPLIMAAQ 116
QY 134 FGEIETVFLLEWGAADPHILAKERESALSLASTGTYDIVG----- 174
DB 120 ENHLEVVKFLLENGANQVATEDGFTPLAVLALQGHENVAHLINVTGKAVRLPALHIA 176
QY 175 -----LLERPDVINDIYDMNGA 191
DB 180 ARNDRTAAVLQNDPNPDLVSKTGFTPLHIAHYENLVNQLLNKRASVNFPTQNGI 236
QY 192 TPLLYAVGNHVKCEALLARGADLTTEADSGYTPMDLVALGYRKVOQVIENH 245

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DB 237 TPLHARSRGVIVWRLLDGAGQIETRTKDELTPHCAARNGHVRISEILLDH 290

RESULT 8

PSDA MOUSE STANDARD; PRT; 231 AA.

ID PSDA_MOUSE 0922X2; 0907N8; Created

AC 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE 26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin).

DE PSMD10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RT "Cloning of mouse gankyrin containing ankyrin repeats."

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue;

RX MEDLINE=2108560; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Catinacci P., de Bonaldo M.F., Brownstein M.O., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -1- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.

CC -1- SUBUNIT: Component of the PA700 complex.

CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.

CC -----

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CC -----

DR EMBL; AB022022; BAA3696.1; -;

DR EMBL; AK009068; BAB2605.1; -;

DR HSSP; P42773; 11H.

DR MGD; MGI:185898; Pemd10.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 5.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SMO0248; ANK; 5.

DR PROSITE; PS50088; ANK_REPEAT; 5.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

KW Proteasome; ANK repeat; Repeat.

FT REPEAT 39 68 ANK 1.

FT REPEAT 72 101 ANK 2.

FT REPEAT 105 134 ANK 3.

FT REPEAT 138 167 ANK 4.

FT REPEAT 171 200 ANK 5.

FT CONFLICT 101 101 A -> S (IN REF. 1).

FT CONFLICT 122 122 A -> S (IN REF. 1).

FT CONFLICT 226 226 G -> S (IN REF. 1).

SO SEQUENCE 231 AA; 25053 MW; BCE7B9A79C8CF588 CRC64;

Query Match 13.6%; Score 182.5; DB 1; Length 231;

Best Local Similarity 31.4%; Pred. No. 86-08;

Matches 54; Conservative 27; Mismatches 86; Indels 5; Gaps 1;

OY 89 LDLSLHQAAGCEIDQKEHRLKGNLVNKRDERFTPLMASAGETVAFLEWCA 148

DB 5 VSNITCNLAYSKDELKERILADKSLATFRDQSRALHMACSGHTEIYFLLQLGV 64

OY 149 PHILAKERESALSLASTGYTDIVGLERDVDTINITYMNGCTPLLYAVRGHVHCVEA 208

DB 65 PVNDKDDAGWSPHLHIAAGRDEIVKALLVKGAHVNAVONCTPLHYASKRHEIAVM 124

OY 209 LIARADLTTEADSGYTPMDLVALGYRKVQGVIEHHIKLFQSNLVPADE 260

DB 125 LLEGANPDADKHVDATAMHRAAKGNLKMV-----HLLFYKASTNIQDTE 171

RESULT 9

YB23_HUMAN STANDARD; PRT; 768 AA.

ID YB23_HUMAN 090LJ7;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein KIAA1223 (Fragment).

GN KIAA1223.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20039619; PubMed=10574462;

RA Nagase T., Ishikawa K.-I., Kikuno R., Hirogawa M., Nomura N., Ohara O.;

RA "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

RL DNA Res. 6:337-345(1999).

CC -1- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.

CC -----

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CC -----

DR EMBL; AB033049; BAA86537.1; -;

DR HSSP; P42771; IDC2.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 14.

DR SMART; SMO0248; ANK; 13.

DR PROSITE; PS50088; ANK_REPEAT; 13.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

KW Hypothetical protein; Repeat; ANK repeat.

FT NON_TER 1 1

FT REPEAT 1 11 ANK 1.

FT REPEAT 15 44 ANK 2.

FT REPEAT 48 82 ANK 3.

FT REPEAT 86 115 ANK 4.

FT REPEAT 119 148 ANK 5.

RESULT 14
Y379_HUMAN

Query Match	12.9%;	Score 172.5;	DB 1;	Length 1059;
Best Local Similarity	22.2%;	Pred. No. 4.3e-06;		
Matches 69; Conservative	43;	Mismatches 110;	Indels 89;	Gaps 9

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QY 22 GDPED-----PGEADGSDTVVLSLPCTEPENPEPD----- 55
DB 25 GDPDEVALIFKEDVNFQDNEKRTPLHAAAYLGDAEIIELLISGARVNAKSKWLTPL 84
QY 56 -----ASVSSPQAGSSLSKSTTLTNROR-----GNEVASLPATLSLS----- 93
DB 85 HRAVASCESEAVOVLKKSADVNARKMOTPLHIAANKAVCAEALVPLLSVNVNDR 144
QY 94 -----IHOIAAGELDOLKEHLRKGDNLVKNKPDERTPLIMASAFGEIETVFLMGA 148
DB 145 AGRTALHHAASGHEGEMVYKLLSRGAN-INAFDKDRRAIHMAVMGHIEVVKLLVSHGA 203
QY 149 DPHILAKRESLSLASTGTYDIDVLLERVDIN-----IYMNKG----- 191
DB 204 EVTCCKDKSKYPLHAAASSGMISVYKLLDLGVDMNEPNAYGNTPLHVACYNQGVVNE 263
QY 192 -----TPLLVAVRGNH-VKCVALLARGADLTTEADSGYTPMDLAVALG 234
DB 264 LIDCAIYNQKNEKGTPLHFAAASHTGALCLLVLVNGADVNKKSKDKTPLHMTALHG 323
QY 235 -YRKVQVNIEN 244
DB 324 RFSRQTIOS 334

RESULT 15
ILK_CAVPO STANDARD; PRT; 451 AA.
AC P57044;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Integrin-linked protein kinase (EC 2.7.1.-) (beta-integrin-linked
DE kinase).
GN ILK.
OS Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NC MCB1_taxid=10141;
RN [1]
RA SEQUENCE FROM N.A.
RA Ishii T.;
RT "Guinea pig beta-integrin-linked kinase.";
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR-PROXIMAL, PROTEIN KINASE REGULATING INTEGRIN-
CC MEDIATED SIGNAL TRANSDUCTION. MAY ACT AS A MEDIATOR OF INSIDE-OUT
CC INTEGRIN SIGNALING. FOCAL ADHESION PROTEIN PART OF THE COMPLEX
CC ILK-PINCH. THIS COMPLEX IS CONSIDERED TO BE ONE OF THE CONVERGENCE
CC POINTS OF INTEGRIN- AND GROWTH FACTOR-SIGNALING PATHWAY. COULD BE
CC IMPLICATED IN MEDIATING CELL ARCHITECTURE, ADHESION TO INTEGRIN
CC SUBSTRATES AND ANCHORAGE-DEPENDENT GROWTH IN EPITHELIAL CELLS.
CC PHOSPHORYLATES BETA-1 AND BETA-3 INTEGRIN SUBUNIT ON SERINE AND
CC THREONINE RESIDUES, BUT ALSO AKT1 AND GSK3B (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH CYTOPLASMIC DOMAIN OF BETA 1 SUBUNIT OF
CC INTEGRIN. COULD ALSO INTERACTS WITH BETA 2, BETA 3 AND/OR BETA 5
CC SUBUNIT OF INTEGRIN. ALSO INTERACTS WITH PINCH AND PARVINS (BY
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- DOMAIN: A PH-LIKE DOMAIN IS INVOLVED IN PHOSPHATIDYLINOSITOL
CC PHOSPHATE BINDING (BY SIMILARITY).
CC -!- PTM: AUTOPHOSPHORYLATED ON SERINE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC
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CC
CC EMBL; AF256520; AAF70501.1; -.

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DR HSPB; 000420; 1AWC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Repeat; ANK repeat.
FT REPEAT 33 62 ANK 1.
FT REPEAT 66 95 ANK 2.
FT REPEAT 99 128 ANK 3.
FT DOMAIN 180 212 PH-LIKE.
FT DOMAIN 193 445 PROTEIN_KINASE.
FT NP_BIND 199 207 ATP (BY SIMILARITY).
FT BINDING 220 220 ATP (BY SIMILARITY).
SQ SEQUENCE 451 AA; 51308 MW; 88EF22C4517DD52B CRC64;

Query Match 12.6%; Score 169.5; DB 1; Length 451;
Best Local Similarity 30.4%; Pred. No. 2,3e-06;
Matches 48; Conservative 33; Mismatches 72; Indels 5; Gaps 2;

QY 100 QGELDOLKEHLRKGDNLVKNKPDERTPLIMASAFGEIETVFLMGAADPHILAKERS 159
DB 10 EGNAAVAVRWLMDNTENDLNGDDHGFSPLHWACREGSAVAVEMLTMRGARIVNWRGDDT 69
QY 160 ALSLAGGYTDIVGILLERVDINIVDMNGGTPLVAVRGNHVKCVALLARGADLTTE 219
DB 70 PHLAASHGHRDVIQKLLQYKADINAVNEHGVNVLHVACFWGQDQVADLVANGALVSTIC 129
QY 220 ADSGYTPMDLAVALGRKVOQVNIENHILKLFQS-NLVP 256
DB 130 NKYGEMPMDRAKA-----PLRELLERAEKMKQGNINRIP 163

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Search completed: March 17, 2003, 16:40:00
Job time : 15 secs